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## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

5

## (i) APPLICANT:

- (A) NAME: ZENECA LIMITED  
(B) STREET: 15 STANHOPE GATE  
(C) CITY: LONDON  
(E) COUNTRY: UNITED KINGDOM  
(F) POSTAL CODE (ZIP): W1Y 6LN  
(G) TELEPHONE: 0171 304 5000  
(H) TELEFAX: 0171 304 5151  
(I) TELEX: 0171 834 2042

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## (ii) TITLE OF INVENTION: PROTEINS

## (iii) NUMBER OF SEQUENCES: 131

## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

25

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30

## (ii) MOLECULE TYPE: other nucleic acid

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGAAGCTTGA AGATGGATAC AGTTGGTGCA GC

32

5 (2) INFORMATION FOR SEQ ID NO: 2:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GGAAGCTTAG ACAGATGGGG GTGTCGTTTT G

31

25 (2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

30

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Ser Gly Ala  
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn  
20 25 30

Tyr Met

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GACATTCAGC TGACCCAGTC TCCA

24

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GACATTGAGC TCACCCAGTC TCCA

24

5 (2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

20 AGGTSMARCT GCAGSAGTCW GG

22

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ACTAGTGGA TTCAGTGTGA GGTSCARCTG CAGCARTCWG G

41

5 (2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

20 GACATTGAGC TCACCCAGTC TCCAGCAATC ATGTCTGCAT CTCCAGGGGA GAAGGTCACC 60

ATAACCTGCA GTGCCAGCTC AAGTGTAAC TACATGCACT GGTTCAGCA GAAGCCAGGC 120

ACTTCTCCCA AACTCTGGAT TTATAGCACA TCCAACCTGG CTTCTGGAGT CCCTGCTCGC 180

25

TTCAGTGGCA GTGGATCTGG GACCTCTTAC TCTCTCACA TCAGCCGAAT GGAGGCTGAA 240

GATGCTGCCA CTTATTACTG CCAGCAAAGG AGTACTTACC CGCTCACGTT CGGTGCTGGG 300

30 ACCAAGCTGG AGCTGAAACG GGCTGATGCT GCACCAACTG TATCCATCTT CAAGCTT 357

(2) INFORMATION FOR SEQ ID NO: 9:

35

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly  
 1 5 10 15

Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met  
 20 25 30

His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp Ile Tyr  
 35 40 45

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser  
 50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu  
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Leu Thr  
 85 90 95

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala  
 100 105

## (2) INFORMATION FOR SEQ ID NO: 10:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs

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- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: other nucleic acid

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GAGGTGCAGC TGCAGCARTC WGGGGCAGAG CTTGTGAGGT CAGGGGCCTC AGTCAAGTTG 60  
TCCTGCACAG CTTCTGGCTT CAACATTAAA GACAACTATA TGCACTGGGT GAAGCAGAGG 120  
CCTGAACAGG GCCTGGAGTG GATTGCATGG ATTGATCCTG AGAATGGTGA TACTGAATAT 180  
GCCCCGAAGT TCCGGGGCAA GGCCACTTTG ACTGCAGACT CATCCTCCAA CACAGCCTAC 240  
CTGCACCTCA GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTACTGTCA TGTCCTGATC 300  
TATGCTGGTT ATTTGGCTAT GGACTACTGG GGTCAAGGAA CCTCAGTCGC CGTCTCCTCA 360

25 (2) INFORMATION FOR SEQ ID NO: 11:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Ser Gly Ala

1 5 10 15

5

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn

20 25 30

Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

10 35 40 45

Ala Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe

50 55 60

15

Arg Gly Lys Ala Thr Leu Thr Ala Asp Ser Ser Ser Asn Thr Ala Tyr

65 70 75 80

Leu His Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys

20 85 90 95

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln

100 105 110

25

Gly Thr Ser Val Ala Val Ser Ser

115 120

(2) INFORMATION FOR SEQ ID NO: 12:

30

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(11) MOLECULE TYPE: other nucleic acid



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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AAGCTTTCCC GCGGGGACAT TGAGCTCACC CAGTCTCCA

39

5 (2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

20 AAGCTTCTCG AGCTTGGTCC CAGCACCGAA

30

(2) INFORMATION FOR SEQ ID NO: 14:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

AAGCTTGGA TTCAGTGTGA GGTGCAGCTG CAGCAG

36

5 (2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

20 AAGCTTCGAG CTCACGGCGA CTGAGGTTCC TTG

33

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 705 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: other nucleic acid

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ATGGATTTTC AAGTGCAGAT TTTCAGCTTC CTGCTAATCA GTGCTTCAGT CATAATGTCC 60

5 CGCGGGGACA TTGAGCTCAC CCAGTCTCCA GCAATCATGT CTGCATCTCC AGGGGAGAAG 120

GTCACCATAA CCTGCAGTGC CAGCTCAAGT GTAACCTTACA TGCACTGGTT CCAGCAGAAG 180

CCAGGCACTT CTCCCAAAT CTGGATTTAT AGCACATCCA ACCTGGCTTC TGGAGTCCCT 240

10 GCTCGCTTCA GTGGCAGTGG ATCTGGGACC TCTTACTCTC TCACAATCAG CCGAATGGAG 300

GCTGAAGATG CTGCCACTTA TTACTGCCAG CAAAGGAGTA CTTACCCGCT CACGTTCCGT 360

15 GCTGGGACCA AGCTCGAGAT CAAACGGACT GTGGCTGCAC CATCTGTCTT CATCTTCCCG 420

CCATCTGATG AGCAGTTGAA ATCTGGAAT GCCTCTGTTG TGTGCCTGCT GAATAACTTC 480

TATCCCAGAG AGGCCAAAGT ACAGTGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC 540

20 CAGGAGAGTG TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCTG 600

ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT CACCCATCAG 660

25 GGCCTGAGTT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG AGTGT 705

(2) INFORMATION FOR SEQ ID NO: 17:

(1) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1				5						10					15
Val	Ile	Met	Ser	Arg	Gly	Asp	Ile	Glu	Leu	Thr	Gln	Ser	Pro	Ala	Ile
				20						25					30
Met	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser
				35						40					45
Ser	Ser	Val	Thr	Tyr	Met	His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Thr	Ser
				50						55					60
Pro	Lys	Leu	Trp	Ile	Tyr	Ser	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
				65						70					75
Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
				85						90					95
Ser	Arg	Met	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Arg
				100						105					110
Ser	Thr	Tyr	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Ile	Lys
				115						120					125
Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu
				130						135					140
Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe
				145						150					155
Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln
				165						170					175
Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser
				180						185					190

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Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu  
 195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser  
 5 210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230 235

## 10 (2) INFORMATION FOR SEQ ID NO: 18:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 765 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

25 ATGAAGTTGT GGCTGAACTG GATTTTCCTT GTAACACTTT TAAATGGAAT TCAGTGTGAG 60  
 GTGCAGCTGC AGCARTCAGG GGCAGAGCTT GTGAGGTCAG GGGCCTCAGT CAAGTTGTCC 120  
 TGCACAGCTT CTGGCTTCAA CATTAAAGAC AACTATATGC ACTGGGTGAA GCAGAGGCCT 180  
 30 GAACAGGGCC TGGAGTGGAT TGCATGGATT GATCCTGAGA ATGGTGATAC TGAATATGCC 240  
 CCGAAGTTCC GGGGCAAGGC CACTTTGACT GCAGACTCAT CCTCCAACAC AGCCTACCTG 300  
 35 CACCTCAGCA GCCTGACATC TGAGGACACT GCCGTCTATT ACTGTCATGT CCTGATCTAT 360  
 GCTGGTTATT TGGCTATGGA CTACTGGGGT CAAGGAACCT CAGTCGCCGT GAGCTCGGCT 420

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AGCACCAAGG GACCATCGGT CTTCCCCCTG GCCCCCTGCT CCAGGAGCAC CTCCGAGAGC 480

ACAGCCGCCC TGGGCTGCCT GGTC AAGGAC TACTTCCCCG AACCGGTGAC GGTGTCGTGG 540

5 AACTCAGGCG CTCTGACCAG CGGCGTGAC ACCTTCCCG CTGTCTTACA GTCCTCAGGA 600

CTCTACTCCC TCAGCAGCGT CGTGACGGTG CCCTCCAGCA ACTTCGGCAC CCAGACCTAC 660

ACCTGCAACG TAGATCACAA GCCCAGCAAC ACCAAGGTGG ACAAGACAGT TGAGCGCAAA 720

10

TGTTGTGTCG AGTGCCCAACC GTGCCCCGCG CCACCTGTGG CCGGC 765

(2) INFORMATION FOR SEQ ID NO: 19:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Met Lys Leu Trp Leu Asn Trp Ile Phe Leu Val Thr Leu Leu Asn Gly

1

5

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Ile Gln Cys Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg

20

25

30

Ser Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile

35

35

40

45

Lys Asp Asn Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu

50

55

60

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Glu Trp Ile Ala Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala  
 65 70 75 80

5 Pro Lys Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Ser Ser Ser Asn  
 85 90 95

Thr Ala Tyr Leu His Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val  
 100 105 110

10 Tyr Tyr Cys His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr  
 115 120 125

Trp Gly Gln Gly Thr Ser Val Ala Val Ser Ser Ala Ser Thr Lys Gly  
 15 130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser  
 145 150 155 160

20 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val  
 165 170 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe  
 180 185 190

25 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val  
 195 200 205

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val  
 30 210 215 220

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys  
 225 230 235 240

35 Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly  
 245 250 255

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(2) INFORMATION FOR SEQ ID NO: 20:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys

1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr

20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser

35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser

50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr

65 70 75 80

Tyr Ile Cys Asn Val Asn His Asn Pro Ser Asn Thr Lys Val Asp Lys

85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys

100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro

115 120



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(2) INFORMATION FOR SEQ ID NO: 21:

5

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 369 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

20

GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCTT CCTCCAAGAG CACCTCTGGG 60

GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG 120

25 TGGAATCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA 180

GGACTCTACT CCCTCAGCAG CGTGGTGACT GTGCCCTCCA GCAGCTTGGG CACCCAGACC 240

TACATCTGCA ACGTGAATCA CAACCCAGC AACACCAAGG TCGACAAGAA AGTTGAGCCC 300

30

AAATCTTGTG ACAAGACGCA CACGTGCCCC CCGTGCCCGG CTCCGGAAGT GCTGGGTGGC 360

CCGTAATAG 369

35 (2) INFORMATION FOR SEQ ID NO: 22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids

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(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg  
1 5 10 15

15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
20 25 30

20

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
50 55 60

25

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr  
65 70 75 80

30

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys  
85 90 95

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
100 105 110

35

Pro Val Ala Gly  
115

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## (2) INFORMATION FOR SEQ ID NO: 23:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 348 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

10

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

15

GCTAGCACCA AGGGACCATC GGTCTTCCCC CTGGCCCCCT GCTCCAGGAG CACCTCCGAG 60

AGCACAGCCG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG 120

20 TGGAACTCAG GCGCTCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA 180

GGACTCTACT CCCTCAGCAG CGTCGTGACG GTGCCCTCCA GCAACTTCGG CACCCAGACC 240

TACACCTGCA ACGTAGATCA CAAGCCCAGC AACACCAAGG TGGACAAGAC AGTTGAGCGC 300

25

AAATGTTGTG TCGAGTGCCC ACCGTGCCCC GCGCCACCTG TGGCCGGC 348

## (2) INFORMATION FOR SEQ ID NO: 24:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

35

## (ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg  
 1 5 10 15  
 5  
 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 20 25 30  
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
 10 35 40 45  
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
 50 55 60  
 15  
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
 65 70 75 80  
 Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
 85 90 95  
 20  
 Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro  
 100 105 110  
 Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg  
 25 115 120 125  
 Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys  
 130 135 140  
 30  
 Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro  
 145 150 155 160  
 Ala Pro Glu Leu Leu Gly Gly  
 165  
 35

(2) INFORMATION FOR SEQ ID NO: 25:

(1) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 501 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: other nucleic acid

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GCTAGCACCA AGGGCCCATC GGTCTTCCCC CTGGCGCCCT GCTCCAGGAG CACCTCTGGG 60  
15 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTGG 120  
TGGAATCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA 180  
GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC 240  
20 TACACCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAG AGTGGAGCTG 300  
AAAACCCAC TTGGTGACAC AACTCACACG TGCCCTAGGT GTCCTGAACC TAAATCTTGT 360  
25 GACACACCTC CCCCCTGCCC ACGGTGCCCC GAGCCCAAAT CTTGCGACAC GCCCCACCG 420  
TGTCCTGAT GTCTGAACC AAAGAGCTGT GACTACTCCAC CGCCCTGCCC GAGGTGCCCC 480  
GCACCTGAAC TCCTGGGAGG A 501

30

(2) INFORMATION FOR SEQ ID NO: 26:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

35

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(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Ser Ala Ser Ser Ser Val Thr Tyr Met His  
1 5 10

10 (2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

25 Ser Thr Ser Asn Leu Ala Ser  
1 5

(2) INFORMATION FOR SEQ ID NO: 28:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: peptide

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

5 Gln Gln Arg Ser Thr Tyr Pro Leu Thr  
1 5

(2) INFORMATION FOR SEQ ID NO: 29:

10

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

25 (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Asp Asn Tyr Met His  
1 5

30 (2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Phe Asn Ile Lys Asp Asn Tyr Met His

1

5

10 (2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe Arg

1

5

10

15

Gly

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear



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(ii) MOLECULE TYPE: peptide

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr

1 5 10

10

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: peptide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

25

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr

1 5 10

(2) INFORMATION FOR SEQ ID NO: 34:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: other nucleic acid

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TCGAGAGATC TAAGCTTCCG CGGGAATTCC TCGAGGAGCT CCCCGGGGGA TCCGTCGACT 60

5

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

20

CTAGAGTCGA CGGATCCCCC GGGGAGCTCC TCGAGGAATT CCCGCGGAAG CTTAGATCTC 60

(2) INFORMATION FOR SEQ ID NO: 36:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

30

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

AAGCTTCCCG GGTATTAAAG CAGAACTTG

29

5 (2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

20 ACTAGTGGAT CCCAGACATG ATAAGATAC

29

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: other nucleic acid

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

GGTCTATATA AGCAGAGCTG TCTGGCTAAC TAGAGAACC

39

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## (2) INFORMATION FOR SEQ ID NO: 39:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GGTTCTCTAG TTAGCCAGAC AGCTCTGCTT ATATAGACC

39

## 15 (2) INFORMATION FOR SEQ ID NO: 40:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

30 GGACTTTCCT ACTTGGCAG

19

## (2) INFORMATION FOR SEQ ID NO: 41:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GGCAACTAGA AGGCACAGTC

20

10

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

25

AGCTTGCCGC CACCATGGAT TTTCAAGTGC AGATTTTCAG CTCCTGCTA ATCAGTGCTT

60

CAGTCATAAT GTCCCGC

77

30 (2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: other nucleic acid

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5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GGGACATTAT GACTGAAGCA CTGATTAGCA GGAAGCTGAA AATCTGCACT TGAAAATCCA 60

TGGTGGCGGC A 71

10

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

25

AGCTTGCCGC CACCATGAAG TTGTGGCTGA ACTGGATTTT CCTTGTAACA CTTTAAATG 60

G 61

30 (2) INFORMATION FOR SEQ ID NO: 45:

(1) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

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5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

AATTCCATTT AAAAGTGTTA CAAGGAAAAT CCAAGTTCAGC CACAACTTCA TGGTGGCGGC 60

A 61

10

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

AAGCTTCTCG AGATCAAACG GACTGTGGCT GCACCATCTG TCTTCATCTT CCCGCCATCT 60

GATGAGCAGT TGAAATCTGG AACTGCCTCT GTTGTGTGCC TGCTGAATAA CTTCTATCCC 120

30 AGAGAGGCCA AAGTACAGTG GAAGGTGGAT AACGCCCTCC AATCGGGTAA CTCCCAGGAG 180

AGTGTCAAG AGCAGGACAG CAAGGACAGC ACCTACAGCC TCAGCAGCAC CCTGACGCTG 240

AGCAAAGCAG ACTACGAGAA ACACAAAGTC TACGCCTGCG AAGTCACCCA TCAGGGCCTG 300

35 AGTTCGCCCC TCACAAAGAG CTTCAACAGG GGAGAGTGTT AATAGCCCGG GACTAGT 357

(2) INFORMATION FOR SEQ ID NO: 47:

- 120 -

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 base pairs

(B) TYPE: nucleic acid

5 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

10

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

15 GGAAGCTTGA GCTCGGCTAG CACCAAGGGA CCATCGGTCT TCCCCCTGGC CCCCTGCTCC 60  
AGGAGCACCT CCGAGAGCAC AGCCGCCCTG GGCTGCCTGG TCAAGGACTA CTTCCCCGAA 120  
CCGGTGACGG TGTCGTGGAA CTCAGGCGCT CTGACCAGCG GCGTGACAC CTTCCCGGCT 180  
20 GTCCTACAGT CCTCAGGACT CTA CTCCCTC AGCAGCGTCG TGACGGTGCC CTCCAGCAAC 240  
TTCGGCACCC AGACCTACAC CTGCAACGTA GATCACAAGC CCAGCAACAC CAAGGTGGAC 300  
25 AAGACAGTTG AGCGCAAATG TTGTGTCGAG TGCCCACCGT GCCCGGCGCC ACCTGTGGCC 360  
GGCTAATAGC CCGGGACTAG T 381

## (2) INFORMATION FOR SEQ ID NO: 48:

30

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 base pairs

(B) TYPE: nucleic acid

35 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid



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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

5 AAGCTTTCCC GCGGCGACAT CCAGATGACC CAGAGCCCAA GCAGCCTGAG CGCTAGCGTG 60  
GGTGACAGAG TGACCATCAC GTGTAGTGCC AGCTCAAGTG TAACTTACAT GCACTGGTAC 120  
CAGCAGAAGC CAGGTAAGGC TCCAAAGCTG CTGATCTACA GCACATCCAA CCTGGCTTCT 180  
10 GGTGTGCCAA GCAGATTCTC CGGAAGCGGT AGCGGCACCG ACTACACCTT CACCATCAGC 240  
AGCCTCCAGC CAGAGGATAT CGCCACCTAC TACTGCCAGC AGAGGAGTAC TTACCCGCTC 300  
ACGTTCCGCC AAGGGACCAA GCTCGAGATC AAACGGACTA GT 342

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 321 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

30 GACATCCAGA TGACCCAGAG CCCAAGCAGC CTGAGCGCTA GCGTGCGTGA CAGAGTGACC 60  
ATCACGTGTA GTGCCAGCTC AAGTGTA ACT TACATGCACT GGTACCAGCA GAAGCCAGGT 120  
35 AAGGCTCCAA AGCTGCTGAT CTACAGCACA TCCAACCTGG CTTCTGGTGT GCCAAGCAGA 180  
TTCTCCGGAA GCGGTAGCGG CACCGACTAC ACCTTCACCA TCAGCAGCCT CCAGCCAGAG 240

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GATATCGCCA CCTACTACTG CCAGCAGAGG AGTACTTACC CGCTCACGTT CGGCCAAGGG 300

ACCAAGCTCG AGATCAAACG G 321

5 (2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

20 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met

20 25 30

25 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr

35 40 45

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser

30 50 55 60

Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu

65 70 75 80

35 Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Leu Thr

85 90 95

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Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg

100

105

(2) INFORMATION FOR SEQ ID NO: 51:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 705 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

10

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

15

ATGGATTTTC AAGTGCAGAT TTTCAGCTTC CTGCTAATCA GTGCTTCAGT CATAATGTCC 60

CGCGGCGACA TCCAGATGAC CCAGAGCCCA AGCAGCCTGA GCGCTAGCGT GGGTGACAGA 120

20 GTGACCATCA CGTGTAGTGC CAGCTCAAGT GTAACCTACA TGCACTGGTA CCAGCAGAAG 180

CCAGGTAAGG CTCCAAAGCT GCTGATCTAC AGCACATCCA ACCTGGCTTC TGGTGTGCCA 240

AGCAGATTCT CCGGAAGCGG TAGCGGCACC GACTACACCT TCACCATCAG CAGCCTCCAG 300

25

CCAGAGGATA TCGCCACCTA CTA CTGCCCAG CAGAGGAGTA CTTACCCGCT CACGTTCCGGC 360

CAAGGGACCA AGCTCGAGAT CAAACGGACT GTGGCTGCAC CATCTGTCTT CATCTTCCCG 420

30 CCATCTGATG AGCAGTTGAA ATCTGGAAC TGCCTCTGTTG TGTGCCTGCT GAATAACTTC 480

TATCCCAGAG AGGCCAAAGT ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC 540

CAGGAGAGTG TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCCTG 600

35

ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT CACCCATCAG 660

GGCCTGAGTT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG AGTGT 705

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## (2) INFORMATION FOR SEQ ID NO: 52:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 235 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## 10 (ii) MOLECULE TYPE: protein

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15

Val Ile Met Ser Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser  
35 40 45

Ser Ser Val Thr Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala  
50 55 60

Pro Lys Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro  
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile  
85 90 95

Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg  
100 105 110

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Ser Thr Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
 115 120 125

5 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu  
 130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe  
 145 150 155 160

10 Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln  
 165 170 175

15 Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser  
 180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu  
 195 200 205

20 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser  
 210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230 235

25 (2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 385 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GAAGCTTGGA ATTCAGTGTG AGGTGCAGCT GCAGCAGAGC GGTCCAGGTC TCGTACGGCC 60

5 TAGCCAGACC CTGAGCCTCA CGTGCACCGC ATCTGGCTTC AACATTAAGG ACAATTACAT 120

GCACTGGGTG AGACAGCCAC CTGGACGAGG CCTTGAGTGG ATTGGATGGA TTGACCCTGA 180

GAATGGTGAC ACTGAGTACG CACCTAAGTT TCGCGGCCGC GTGACAATGC TGGCAGACAC 240

10 TAGTAAGAAC CAGTTCAGCC TGAGACTCAG CAGCGTGACA GCCGCCGACA CCGCGGTCTA 300

TTATTGTCAC GTCCTGATAT ACGCCGGGTA TCTGGCAATG GACTACTGGG GCCAAGGGAC 360

15 CCTCGTCACC GTGAGCTCGA CTAGT 385

(2) INFORMATION FOR SEQ ID NO: 54:

(1) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25 (11) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

30 GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60

ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120

CCTGGACGAG GCCTTGAGTG GATTGGATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180

35 GCACCTAAGT TTCGCGGCCG CGTGACAATG CTGGCAGACA CTAGTAAGAA CCAATTTCAGC 240

CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300

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TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360

## 5 (2) INFORMATION FOR SEQ ID NO: 55:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 120 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

20 Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn  
20 25 30

25 Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile  
35 40 45

30 Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe  
50 55 60

Arg Gly Arg Val Thr Met Leu Ala Asp Thr Ser Lys Asn Gln Phe Ser  
65 70 75 80

35 Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

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His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

5

115

120

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 765 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

ATGAAGTTGT GGCTGAACTG GATTTTCCTT GTAACACTTT TAAATGGAAT TCAAGTGTGAG 60

GTGCAGCTGC AGCAGAGCGG TCCAGGTCTC GTACGGCCTA GCCAGACCCT GAGCCTCAGC 120

25

TGACCCGCAT CTGGCTTCAA CATTAAGGAC AATTACATGC ACTGGGTGAG ACAGCCACCT 180

GGACGAGGCC TTGAGTGGAT TGGATGGATT GACCCTGAGA ATGGTGACAC TGAGTACGCA 240

30

CCTAAGTTTC GCGGCCGCGT GACAATGCTG GCAGACACTA GTAAGAACCA GTTCAGCCTG 300

AGACTCAGCA GCGTGACAGC CGCCGACACC GCGGTCTATT ATTGTCACGT CCTGATATAC 360

GCCGGGTATC TGGCAATGGA CTAAGGGGGC CAAGGGACCC TCGTCACCGT GAGCTCGGCT 420

35

AGCACCAAGG GACCATCGGT CTTCCCCCTG GCCCCCTGCT CCAGGAGCAC CTCCGAGAGC 480

ACAGCCGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC GGTGTCGTGG 540



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AACTCAGGCG CTCTGACCAG CGGCGTGAC ACCTTCCCGG CTGTCCTACA GTCCTCAGGA 600  
CTCTACTCCC TCAGCAGCGT CGTGACGGTG CCCTCCAGCA ACTTCGGCAC CCAGACCTAC 660  
5 ACCTGCAACG TAGATCACAA GCCCAGCAAC ACCAAGGTGG ACAAGACAGT TGAGCGCAAA 720  
TGTTGTGTGG AGTGCCCAAC GTGCCCCGGC CCACCTGTGG CCGGC 765

10 (2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids  
(B) TYPE: amino acid  
15 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

25 Met Lys Leu Trp Leu Asn Trp Ile Phe Leu Val Thr Leu Leu Asn Gly  
1 5 10 15  
Ile Gln Cys Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg  
20 25 30  
30 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile  
35 40 45  
Lys Asp Asn Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu  
50 55 60  
Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala  
65 70 75 80

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Pro Lys Phe Arg Gly Arg Val Thr Met Leu Ala Asp Thr Ser Lys Asn

85

90

95

5 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val

100

105

110

Tyr Tyr Cys His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr

115

120

125

10

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly

130

135

140

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser

15

145

150

155

160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

165

170

175

20

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

180

185

190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

195

200

205

25

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val

210

215

220

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys

30

225

230

235

240

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly

245

250

255

35 (2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GGCGACATCC AGCTGACCCA GAGCCCAAGC AGCCTGAGCG

40

10

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

25

CTAGCGCTCA GGCTGCTTGG GCTCTGGGTC AGCTGGATGT CGCCGC

46

(2) INFORMATION FOR SEQ ID NO: 60:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: other nucleic acid

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

GACATCCAGC TGACCCAGAG CCCAAGCAGC CTGAGCGCTA GCGTGGGTGA CAGAGTGACC 60  
5 ATCACGTGTA GTGCCAGCTC AAGTGTAAC TACATGCACT GGTACCAGCA GAAGCCAGGT 120  
AAGGCTCCAA AGCTGCTGAT CTACAGCACA TCCAACCTGG CTTCTGGTGT GCCAAGCAGA 180  
TTCTCCGGAA GCGGTAGCGG CACCGACTAC ACCTTCACCA TCAGCAGCCT CCAGCCAGAG 240  
10 GATATCGCCA CCTACTACTG CCAGCAGAGG AGTACTTACC CGCTCACGTT CGGCCAAGGG 300  
ACCAAGCTCG AGATCAAACG G 321

15 (2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

30 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met  
20 25 30

35 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr  
35 40 45

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Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser  
50 55 60

5 Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu  
65 70 75 80

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Leu Thr  
85 90 95

10 Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg  
100 105

(2) INFORMATION FOR SEQ ID NO: 62:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: other nucleic acid

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

GGCCAGATCG TGCTGACCCA GAGCCCAAGC AGCCTGAGCG

40

30 (2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: other nucleic acid

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5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

CTAGCGCTCA GGCTGCTTGG GCTCTGGGTC AGCAGGATCT GGCCGC

46

(2) INFORMATION FOR SEQ ID NO: 64:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

CAGATCGTGC TGACCCAGAG CCCAAGCAGC CTGAGCGCTA GCGTGGGTGA CAGAGTGACC 60

25

ATCACGTGTA GTGCCAGCTC AAGTGTAAC TACATGCACT GGTACCAGCA GAAGCCAGGT 120

AAGGCTCCAA AGCTGCTGAT CTACAGCACA TCCAACCTGG CTTCTGGTGT GCCAAGCAGA 180

30 TTCTCCGAA GCGGTAGCGG CACCGACTAC ACCTTCACCA TCAGCAGCCT CCAGCCAGAG 240

GATATCGCCA CCTACTACTG. CCAGCAGAGG AGTACTTACC CGCTCACGTT CGGCCAAGGG 300

ACCAAGCTCG AGATCAAACG G 321

35

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- 135 -

- (A) LENGTH: 107 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: protein

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

Gln Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15

15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met  
 20 25 30

20

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr  
 35 40 45

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser  
 50 55 60

25

Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu  
 65 70 75 80

30

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Leu Thr  
 85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg  
 100 105

35 (2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

- 136 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: other nucleic acid

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

CGTATTAGTC ATCGCTATTA CC

22

(2) INFORMATION FOR SEQ ID NO: 67:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

GTTGGATGTG CTGTAGATCC ACAGCTTTGG AGCCTTACC

39

(2) INFORMATION FOR SEQ ID NO: 68:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: other nucleic acid



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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

5

TCCGTTTGAT CTCGAGCTTG G

21

(2) INFORMATION FOR SEQ ID NO: 69:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GGTAAGGCTC CAAAGCTGTG GATCTACAGC ACATCCAAC

39

25 (2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs

(B) TYPE: nucleic acid

30

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

35

- 138 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

GACATCCAGA TGACCCAGAG CCCAAGCAGC CTGAGCGCTA GCGTGGGTGA CAGAGTGACC 60  
 5 ATCACGTGTA GTGCCAGCTC AAGTGTAAC TACATGCACT GGTACCAGCA GAAGCCAGGT 120  
 AAGGCTCCAA AGCTGTGGAT CTACAGCACA TCCAACCTGG CTTCTGGTGT GCCAAGCAGA 180  
 TTCTCCGGAA GCGGTAGCGG CACCGACTAC ACCTTCACCA TCAGCAGCCT CCAGCCAGAG 240  
 10 GATATCGCCA CCTACTACTG CCAGCAGAGG AGTACTTACC CGCTCACGTT CGGCCAAGGS 300  
 ACCAAGCTCG AGATCAAACG G 321

15 (2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

30 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met  
 20 25 30

35 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr  
 35 40 45

- 139 -

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser  
 50 55 60

Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu  
 5 65 70 75 80

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Leu Thr  
 85 90 95

10 Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg  
 100 105

(2) INFORMATION FOR SEQ ID NO: 72:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: other nucleic acid

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

CCTTGAGTGG ATTGCATGGA TTGACCCTGA GAATGGTGAC ACTGAGTACG CACCTAAGTT 60

30 TCGC 64

(2) INFORMATION FOR SEQ ID NO: 73:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid

- 140 -

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

10

GGCCGCGAAA CTTAGGTGCG TACTCAGTGT CACCATTCTC AGGGTCAATC CATGCAATCC 60

ACTCAAGG 68

15 (2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

30 GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60

ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120

CCTGGACGAG GCCTTGAGTG GATTGCATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180

35

GCACCTAAGT TTCGCGGCCG CGTGACAATG CTGGCAGACA CTAGTAAGAA CCAGTTCAGC 240

CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300

- 141 -

TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360

## (2) INFORMATION FOR SEQ ID NO: 75:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

10

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

20

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn

20 25 30

25

Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile

35 40 45

Ala Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe

50 55 60

30

Arg Gly Arg Val Thr Met Leu Ala Asp Thr Ser Lys Asn Gln Phe Ser

65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys

35

85 90 95

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln

100 105 110

- 142 -

Gly Thr Leu Val Thr Val Ser Ser

115

120

## 5 (2) INFORMATION FOR SEQ ID NO: 76:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

20 GGCCGCGTGA CAATGCTGGC AGACTCAAGT AAGAACCAGG CCAGCCTGAG ACTCAGCAGC 60  
GTGACAGCCG CCGACACCGC 80

## (2) INFORMATION FOR SEQ ID NO: 77:

25

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

30

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GGTGTGGGCG GCTGTCACGC TGCTGAGTCT CAGGCTGGCC TGTTCTTAC TTGAGTCTGC 60

5 CAGCATTGTC ACGC 74

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid

15

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

25 GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60

ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120

CCTGGACGAG GCCTTGAGTG GATTGGATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180

30

GCACCTAAGT TTCGCGGCCG CGTGACAATG CTGGCAGACT CAAGTAAGAA CCAGGCCAGC 240

CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300

35 TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360

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## (2) INFORMATION FOR SEQ ID NO: 79:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn  
 20 25 30

Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile  
 35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe  
 50 55 60

Arg Gly Arg Val Thr Met Leu Ala Asp Ser Ser Lys Asn Gln Ala Ser  
 65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
 115 120



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## (2) INFORMATION FOR SEQ ID NO: 80:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 360 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## 10 (ii) MOLECULE TYPE: other nucleic acid

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60  
ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120  
20 CCTGGACGAG GCCTTGAGTG GATTGCATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180  
GCACCTAAGT TTCGCGGCCG CGTGACAATG CTGGCAGACT CAAGTAAGAA CCAGGCCAGC 240  
25 CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300  
TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360

## 30 (2) INFORMATION FOR SEQ ID NO: 81:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 120 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

5

1                      5                      10                      15

[illegible]

Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile

35                      40                      45

50                      55                      60

Arg Gly Arg Val Thr Met Leu Ala Asp Ser Ser Lys Asn Gln Ala Ser

65                      70                      75                      80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys

**85                      90                      95**

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln

100                      105                      110

Gly Thr Leu Val Thr Val Ser Ser

115 120

(2) INFORMATION FOR SEQ ID NO: 82:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: other nucleic acid

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

5

GGCCGCGCCA CAATGCTGGC AGACACTAGT AAGAACCAGT TCAGCCTGAG ACTCAGCAGC 60

GTGACAGCCG CCGACACCGC 80

10 (2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 base pairs

(B) TYPE: nucleic acid

15

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

25 GGTGTCGGCG GCTGTCACGC TGCTGAGTCT CAGGCTGAAC TGGTTCTTAC TAGTGTCTGC 60

CAGCATTGTG GCGC 74

(2) INFORMATION FOR SEQ ID NO: 84:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

35

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

"PCT/GB97/01165"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

5 GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60  
 ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120  
 CCTGGACGAG GCCTTGAGTG GATTGGATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180  
 10 GCACCTAAGT TTCGCGGCCG CGCCACAATG CTGGCAGACA CTAGTAAGAA CCAGTTCAGC 240  
 CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300  
 TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360

15

(2) INFORMATION FOR SEQ ID NO: 85:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 120 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln  
 1 5 10 15

35 Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn  
 20 25 30

- 149 -

Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile

35

40

45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe

5

50

55

60

Arg Gly Arg Ala Thr Met Leu Ala Asp Thr Ser Lys Asn Gln Phe Ser

65

70

75

80

10

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys

85

90

95

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln

100

105

110

15

Gly Thr Leu Val Thr Val Ser Ser

115

120

(2) INFORMATION FOR SEQ ID NO: 86:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

25

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

GGCCGCGCCA CAATGCTGGC AGACTCAAGT AAGAACCAGG CCAGCCTGAG ACTCAGCAGC

60

35

GTGACAGCCG CCGACACCGC

80

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## (2) INFORMATION FOR SEQ ID NO: 87:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

GGTGTGCGCG GCTGTCACGC TGCTGAGTCT CAGGCTGGCC TGGTTCTTAC TTGAGTCTGC 60  
CAGCATTGTG GCGC 74

## (2) INFORMATION FOR SEQ ID NO: 88:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60  
ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120

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CCTGGACGAG GCCTTGAGTG GATTGGATGG ATGACCCTG AGAATGGTGA CACTGAGTAC 180

GCACCTAAGT TTCGCGGCCG CGCCACAATG CTGGCAGACT CAAGTAAGAA CCAGGCCAGC 240

5 CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300

TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360

10 (2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

25 Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn  
20 25 30

30

Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile  
35 40 45

35

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe  
50 55 60

Arg Gly Arg Ala Thr Met Leu Ala Asp Ser Ser Lys Asn Gln Ala Ser  
65 70 75 80

- 152 -

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys

85

90

95

5 His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

10

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: other nucleic acid

20

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

25

GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60

ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120

30 CCTGGACGAG GCCTTGAGTG GATTGCATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180

GCACCTAAGT TTCGCGGCCG CGCCACAATG CTGGCAGACT CAAGTAAGAA CCAGGCCAGC 240

CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300

35

TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360



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(2) INFORMATION FOR SEQ ID NO: 91:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn  
 20 25 30

Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile  
 35 40 45

Ala Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe  
 50 55 60

Arg Gly Arg Ala Thr Met Leu Ala Asp Ser Ser Lys Asn Gln Ala Ser  
 65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
 115 120

- 154 -

(2) INFORMATION FOR SEQ ID NO: 92:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 780 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: other nucleic acid

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

15  
ATGAAGTGT GGCTGAACTG GATTTTCCTT GTAACACTTT TAAATGGAAT TCAGTGTGAG 60  
GTGCAGCTGC AGCAGAGCGG TCCAGGTCTC GTACGGCCTA GCCAGACCCT GAGCCTCAGC 120  
20 TGCACCGCAT CTGGCTTCAA CATTAAAGGAC AATTACATGC ACTGGGTGAG ACAGCCACCT 180  
GGACGAGGCC TTGAGTGGAT TGGATGGATT GACCCTGAGA ATGGTGACAC TGAGTACGCA 240  
CCTAAGTTTC GCGGCCGCGT GACAATGCTG GCAGACACTA GTAAGAACCA GTTCAGCCTG 300  
25 AGACTCAGCA GCGTGACAGC CGCCGACACC GCGGTCTATT ATTGTCACGT CCTGATATAC 360  
GCCGGGTATC TGGCAATGGA CTACTGGGGC CAAGGGACCC TCGTCACCGT GAGCTCGGCC 420  
30 TCCACCAAGG GCCCATCGGT CTTCCCCCTG GCACCCTCCT CCAAGAGCAC CTCTGGGGGC 480  
ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC GGTGTCGTGG 540  
AACTCAGGCG CCCTGACCAG CGGCGTGAC ACCTTCCCCG CTGTCCTACA GTCCTCAGGA 600  
35 CTCTACTCCC TCAGCAGCGT GGTGACTGTG CCCTCCAGCA GCTTGGGCAC CCAGACCTAC 660  
ATCTGCAACG TGAATCACAA CCCCAGCAAC ACCAAGGTCG ACAAGAAAGT TGAGCCCCAA 720

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TCTTGTGACA AGACGCACAC GTGCCC GCCG TGCCCGGCTC CGGAAGTCT GGGTGGCCCCG 780

## 5 (2) INFORMATION FOR SEQ ID NO: 93:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

20

Met Lys Leu Trp Leu Asn Trp Ile Phe Leu Val Thr Leu Leu Asn Gly  
1 5 10 15

Ile Gln Cys Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg  
20 25 30

25

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile  
35 40 45

30

Lys Asp Asn Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu  
50 55 60

Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala  
65 70 75 80

35

Pro Lys Phe Arg Gly Arg Val Thr Met Leu Ala Asp Thr Ser Lys Asn  
85 90 95

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Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
 100 105 110

Tyr Tyr Cys His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr  
 5 115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
 130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly  
 10 145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val  
 15 165 170 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe  
 180 185 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val  
 20 195 200 205

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val  
 210 215 220

Asn His Asn Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys  
 25 225 230 235 240

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu  
 245 250 255

30 Leu Gly Gly Pro  
 260

(2) INFORMATION FOR SEQ ID NO: 94:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 918 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

10

ATGAAGTTGT GGCTGAACTG GATTTTCCTT GTAACACTTT TAAATGGAAT TCAGTGTGAG 60

GTGCAGCTGC AGCAGAGCGG TCCAGGTCTC GTACGGCCTA GCCAGACCCT GAGCCTCACG 120

15 TGCACCGCAT CTGGCTTCAA CATTAGGAC AATTACATGC ACTGGGTGAG ACAGCCACCT 180

GGACGAGGCC TTGAGTGGAT TGGATGGATT GACCCTGAGA ATGGTGACAC TGAGTACGCA 240

CCTAAGTTTC GCGGCCGCGT GACAATGCTG GCAGACACTA GTAAGAACCA GTTCAGCCTG 300

20

AGACTCAGCA GCGTGACAGC CGCCGACACC GCGGTCTATT ATTGTCACGT CCTGATATAC 360

GCCGGGTATC TGGCAATGGA CTACTGGGGC CAAGGGACCC TCGTCACCGT GAGCTCGGCT 420

25 AGCACCAAGG GCCCATCGGT CTTCCCCCTG GCGCCCTGCT CCAGGAGCAC CTCTGGGGGC 480

ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC GGTGTCGTGG 540

AACTCAGGCG CCCTGACCAG CGGCGTGCAC ACCTTCCCGG CTGTCCTACA GTCCTCAGGA 600

30

CTCTACTCCC TCAGCAGCGT GGTGACCGTG CCCTCCAGCA GCTTGGGCAC CCAGACCTAC 660

ACCTGCAACG TGAATCACAA GCCCAGCAAC ACCAAGGTGG ACAAGAGAGT GGAGCTGAAA 720

35 ACCCCACTCG GTGACACAAC TCACACGTGC CCTAGGTGTC CTGAACCTAA ATCTTGTGAC 780

ACACCTCCCC CGTGCCACG GTGCCAGAG CCCAAATCTT GCGACACGCC CCCACCGTGT 840

	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2
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CCCAGATGTC CTGAACCAAA GAGCTGTGAC ACTCCACCGC CCTGCCCCGAG GTGCCCAGCA 900

CCTGAACTCC TGGGAGGG 918

5 (2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 306 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

20 Met Lys Leu Trp Leu Asn Trp Ile Phe Leu Val Thr Leu Leu Asn Gly  
 1 5 10 15

Ile Gln Cys Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg  
 20 25 30

25 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile  
 35 40 45

30 Lys Asp Asn Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu  
 50 55 60

Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala  
 65 70 75 80

35

Pro Lys Phe Arg Gly Arg Val Thr Met Leu Ala Asp Thr Ser Lys Asn  
 85 90 95

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Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
 100 105 110

5 Tyr Tyr Cys His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr  
 115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
 130 135 140

10 Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Gly Gly  
 145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val  
 15 165 170 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe  
 180 185 190

20 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val  
 195 200 205

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Thr Cys Asn Val  
 210 215 220

25 Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Leu Lys  
 225 230 235 240

Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys Pro Glu Pro  
 30 245 250 255

Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys  
 260 265 270

35 Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser  
 275 280 285

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Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu  
290 295 300

5 Gly Gly  
305

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 705 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: other nucleic acid

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

ATGGATTTTC AAGTGCAGAT TTTCAGCTTC CTGCTAATCA GTGCTTCAGT CATAATGTCC 60  
CGCGGCCAGA TCGTGCTGAC CCAGAGCCCA AGCAGCCTGA GCGCTAGCGT GGGTGACAGA 120  
25 GTGACCATCA CGTGTAGTGC CAGCTCAAGT GTAACCTACA TGCACTGGTA CCAGCAGAAG 180  
CCAGGTAAGG CTCCAAAGCT GCTGATCTAC AGCACATCCA ACCTGGCTTC TGGTGTGCCA 240  
30 AGCAGATTCT CCGGAAGCGG TAGCGGCACC GACTACACCT TCACCATCAG CAGCCTCCAG 300  
CCAGAGGATA TCGCCACCTA CTA CTGCCCAG CAGAGGAGTA CTTACCCGCT CACGTTCCGC 360  
CAAGGGACCA AGCTCGAGAT CAAACGGACT GTGGCTGCAC CATCTGTCTT CATCTTCCCG 420  
35 CCATCTGATG AGCAGTTGAA ATCTGGAAGT GCCTCTGTTG TGTGCCTGCT GAATAACTTC 480  
TATCCCAGAG AGGCCAAAGT ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC 540



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CAGGAGAGTG TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCCTG 600

ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT CACCCATCAG 660

5

GGCCTGAGTT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG AGTGT 705

(2) INFORMATION FOR SEQ ID NO: 97:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15

25

Val Ile Met Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ser Ser  
20 25 30

30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser  
35 40 45

Ser Ser Val Thr Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala  
50 55 60

35

Pro Lys Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro  
65 70 75 80

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Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile  
 85 90 95

Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg  
 5 100 105 110

Ser Thr Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
 115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu  
 10 130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe  
 145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln  
 15 165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser  
 20 180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu  
 195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser  
 25 210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230 235

30

(2) INFORMATION FOR SEQ ID NO: 98:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

35

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(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

ATGGATTTTC AAGTGCAGAT TTTCAGCTTC CTGCTAATCA GTGCTTCAGT CATAATGTCC 60

10 CGCGGCGACA TCCAGATGAC CCAGAGCCCCA AGCAGCCTGA GCGCTAGCGT GGGTGACAGA 120

GTGACCATCA CGTGTAGTGC CAGCTCAAGT GTAACCTTACA TGCACTGGTA CCAGCAGAAG 180

CCAGGTAAGG CTCCAAAGCT GTGGATCTAC AGCACATCCA ACCTGGCTTC TGGTGTGCCA 240

15 AGCAGATTCT CCGGAAGCGG TAGCGGCACC GACTACACCT TCACCATCAG CAGCCTCCAG 300

CCAGAGGATA TCGCCACCTA CTA CTGCTG CAGAGGAGTA CTTACCCGCT CAGGTTCCGC 360

20 CAAGGGACCA AGCTCGAGAT CAAACGGACT GTGGCTGCAC CATCTGTCTT CATCTTCCCG 420

CCATCTGATG AGCAGTTGAA ATCTGGAAC TGCCTCTGTTG TGTGCCTGCT GAATAACTTC 480

TATCCAGAG AGGCCAAAGT ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC 540

25 CAGGAGAGTG TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCTG 600

ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT CACCCATCAG 660

30 GGCCTGAGTT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG AGTGT 705

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

10 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
 1 5 10 15  
 Val Ile Met Ser Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
 20 25 30  
 15 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser  
 35 40 45  
 Ser Ser Val Thr Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala  
 50 55 60  
 20 Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro  
 65 70 75 80  
 Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile  
 25 85 90 95  
 Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg  
 100 105 110  
 30 Ser Thr Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
 115 120 125  
 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu  
 130 135 140  
 35 Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe  
 145 150 155 160

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Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln  
165 170 175

5 Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser  
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu  
195 200 205

10 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser  
210 215 220

15 Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
225 230 235

(2) INFORMATION FOR SEQ ID NO: 100:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: other nucleic acid

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

CCCAGCACCT GAATCCTGG GAGGAGCAAC AGGACACAGT TATGAGAAGT ACAA

54

(2) INFORMATION FOR SEQ ID NO: 101:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

10 GGGGGTCTAG ATTATTAGTA CAGGTGTTCC AGGACGTAGC TGGCAACATA

50

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

25

GGGGGAGCTC GGCTAGCACC AAGGGCCCAT CGGTCTTCCC CCTGGC

46

(2) INFORMATION FOR SEQ ID NO: 103:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: other nucleic acid

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

TTGTACTTCT CATAACTGTG TCCTGTTGCT CCTCCCAGGA GTTCAGGTGC TGGGC

55

5 (2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

20 GCCTGTGCTC AATATTGATG G

21

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: other nucleic acid

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

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GGAGAAAGCC ATATCTGCCT G

21

(2) INFORMATION FOR SEQ ID NO: 106:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

TCGCTATTAC CATGGTGATG CGGTTTGGC

30

20 (2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: other nucleic acid

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

GGCTGGATTG TCACTGGCGA CTT

23

35

(2) INFORMATION FOR SEQ ID NO: 108:



- 169 -

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

CACAAACAGAG GCAGTTCC

## (2) INFORMATION FOR SEQ ID NO: 109:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CACCTTCACC ATCAGCAGCC

## (2) INFORMATION FOR SEQ ID NO: 110:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

- 170 -

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

10 GGACCTGCTG CAGAGTCTG

19

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

GGCTGCAGGA ATTCTTATTA TAGACGAACC CGGCTATCAA ACTGAGC

47

(2) INFORMATION FOR SEQ ID NO: 112:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1870 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

35

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

AAGCTTGCCG CCACCATGAA GTTGTGGCTG AACTGGATTT TCCTTGTAAC ACTTTTAAAT 60

5 GGAATTCAGT GTGAGGTGCA GCTGCAGCAG AGCGGTCCAG GTCTCGTACG GCCTAGCCAG 120

ACCCTGAGCC TCACGTGCAC CGCATCTGGC TTCAACATTA AGGACAATTA CATGCACTGG 180

GTGAGACAGC CACCTGGACG AGGCCTTGAG TGGATTGGAT GGATTGACCC TGAGAATGGT 240

10 GACACTGAGT ACGCACCTAA GTTTCGCGGC CGCGTGACAA TGCTGGCAGA CACTAGTAAG 300

AACCAGTTCA GCCTGAGACT CAGCAGCGTG ACAGCCGCCG ACACCGCGGT CTATTATTGT 360

15 CACGTCCTGA TATACGCCGG GSTATCTGGCA ATGGACTACT GGGGCCAAGG GACCCTCGTC 420

ACCGTGAGCT CGGCTAGCAC CAAGGGCCCA TCGGTCTTCC CCCTGGCGCC CTGCTCCAGG 480

AGCACCTCTG GGGGCACAGC GGCCCTGGGC TGCCTGGTCA AGGACTACTT CCCC GAACCG 540

20 GTGACGGTGT CGTGGAATC AGGCGCCCTG ACCAGCGGCG TGCACACCTT CCCGGCTGTC 600

CTACAGTCCT CAGGACTCTA CTCCTCAGC AGCGTGGTGA CCGTGCCCTC CAGCAGCTTG 660

25 GGCACCCAGA CCTACACCTG CAACGTGAAT CACAAGCCCA GCAACACCAA GGTGGACAAG 720

AGAGTGGAGC TGAAAACCCC ACTCGGTGAC ACAACTCACA CGTGCCCTAG GTGTCCTGAA 780

CCTAAATCTT GTGACACACC TCCCCGTGC CCACGGTGCC CAGAGCCCAA ATCTTGCGAC 840

30 ACGCCCCCAC CGTGTCCCAG ATGTCCTGAA CCAAAGAGCT GTGACACTCC ACCGCCCTGC 900

CCGAGGTGCC CAGCACCTGA ACTCCTGGGA GGAGCAACAG GACACAGTTA TGAGAAGTAC 960

35 AACAAAGTGG AAACGATAGA GGCTTGGACT CAACAAGTCG CCACTGAGAA TCCAGCCCTC 1020

ATCTCTCGCA GTGTTATCGG AACCACATTT GAGGGACGCG CTATTTACCT CCTGAAGGTT 1080

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GGCAAAGCTG GACAAAATAA GCCTGCCATT TTCATGGACT GTGGTTTCCA TGCCAGAGAG 1140

TGGATTTCTC CTGCATTCTG CCAGTGGTTT GTAAGAGAGG CTGTTTCGTAC CTATGGACGT 1200

5 GAGATCCAAG TGACAGAGCT TCTCGACAAG TTAGACTTTT ATGTCCTGCC TGTGCTCAAT 1260

ATTGATGGCT ACATCTACAC CTGGACCAAG AGCCGATTTT GGAGAAAGAC TCGCTCCACC 1320

CATACTGGAT CTAGCTGCAT TGGCACAGAC CCCAACAGAA ATTTTGATGC TGGTTGGTGT 1380

10 GAAATTGGAG CCTCTCGAAA CCCCTGTGAT GAAACTTACT GTGGACCTGC CGCAGAGTCT 1440

GAAAAGGAGA CCAAGGCCCT GGCTGATTTC ATCCGCAACA AACTCTCTTC CATCAAGGCA 1500

15 TATCTGACAA TCCACTCGTA CTCCCAAATG ATGATCTACC CTTACTCATA TGCTTACAAA 1560

CTCGGTGAGA ACAATGCTGA GTTGAATGCC CTGGCTAAAG CTACTGTGAA AGAACTTGCC 1620

TCACTGCACG GCACCAAGTA CACATATGGC CCGGGAGCTA CAACAATCTA TCCTTCTGCT 1680

20 GGGACTTCTA AAGACTGGGC TTATGACCAA GGAATCAGAT ATTCCTTCAC CTTTGAACCT 1740

CGAGATACAG GCAGATATGG CTTTCTCCTT CCAGAATCCC AGATCCGGGC TACCTGCGAG 1800

25 GAGACCTTCC TGGCAATCAA GTATGTTGCC AGCTACGTCC TGGAACACCT GTACTAATAA 1860

TCTAGAGAGA 1870.

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 613 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- 173 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Met Lys Leu Trp Leu Asn Trp Ile Phe Leu Val Thr Leu Leu Asn Gly

1 5 10 15

5

Ile Gln Cys Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg

20 25 30

10

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile

35 40 45

Lys Asp Asn Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu

50 55 60

15

Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala

65 70 75 80

Pro Lys Phe Arg Gly Arg Val Thr Met Leu Ala Asp Thr Ser Lys Asn

85 90 95

20

Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val

100 105 110

Tyr Tyr Cys His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr

115 120 125

25

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly

130 135 140

30

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Gly Gly

145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

165 170 175

35

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

180 185 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val  
195 200 205

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Thr Cys Asn Val  
5           210                   215                   220

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Leu Lys  
225                    230                    235                    240

10 Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys Pro Glu Pro  
245 250 255

Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys  
260 265 270

15

Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser

275 280 285

Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu  
20                    290                    295                    300

Gly Gly Ala Thr Gly His Ser Tyr Glu Lys Tyr Asn Lys Trp Glu Thr  
305                    310                    315                    320

25 Ile Glu Ala Trp Thr Gln Gln Val Ala Thr Glu Asn Pro Ala Leu Ile  
325 330 335

Ser Arg Ser Val Ile Gly Thr Thr Phe Glu Gly Arg Ala Ile Tyr Leu  
340 345 350

30

Leu Lys Val Gly Lys Ala Gly Gln Asn Lys Pro Ala Ile Phe Met Asp

355 360 365

35 Cys Gly Phe His Ala Arg Glu Trp Ile Ser Pro Ala Phe Cys Gln Trp  
370 375 380

- 175 -

Phe Val Arg Glu Ala Val Arg Thr Tyr Gly Arg Glu Ile Gln Val Thr  
 385 390 395 400

5 Glu Leu Leu Asp Lys Leu Asp Phe Tyr Val Leu Pro Val Leu Asn Ile  
 405 410 415

Asp Gly Tyr Ile Tyr Thr Trp Thr Lys Ser Arg Phe Trp Arg Lys Thr  
 420 425 430

10 Arg Ser Thr His Thr Gly Ser Ser Cys Ile Gly Thr Asp Pro Asn Arg  
 435 440 445

15 Asn Phe Asp Ala Gly Trp Cys Glu Ile Gly Ala Ser Arg Asn Pro Cys  
 450 455 460

Asp Glu Thr Tyr Cys Gly Pro Ala Ala Glu Ser Glu Lys Glu Thr Lys  
 465 470 475 480

20 Ala Leu Ala Asp Phe Ile Arg Asn Lys Leu Ser Ser Ile Lys Ala Tyr  
 485 490 495

Leu Thr Ile His Ser Tyr Ser Gln Met Met Ile Tyr Pro Tyr Ser Tyr  
 500 505 510

25 Ala Tyr Lys Leu Gly Glu Asn Asn Ala Glu Leu Asn Ala Leu Ala Lys  
 515 520 525

Ala Thr Val Lys Glu Leu Ala Ser Leu His Gly Thr Lys Tyr Thr Tyr  
 530 535 540

30 Gly Pro Gly Ala Thr Thr Ile Tyr Pro Ser Ala Gly Thr Ser Lys Asp  
 545 550 555 560

35 Trp Ala Tyr Asp Gln Gly Ile Arg Tyr Ser Phe Thr Phe Glu Leu Arg  
 565 570 575

Asp Thr Gly Arg Tyr Gly Phe Leu Leu Pro Glu Ser Gln Ile Arg Ala  
 580 585 590

- 176 -

Thr Cys Glu Glu Thr Phe Leu Ala Ile Lys Tyr Val Ala Ser Tyr Val

595

600

605

5 Leu Glu His Leu Tyr

610

(2) INFORMATION FOR SEQ ID NO: 114:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

His His Gly Gly Glu His Phe Glu Gly Glu Lys Val Phe Arg Val Asn

1

5

10

15

25 Val Glu Asp Glu Asn His Ile Asn Ile Ile Arg Glu Leu Ala Ser Thr

20

25

30

Thr Gln Ile Asp Phe Trp Lys Pro Asp Ser Val Thr Gln Ile Lys Pro

35

40

45

30

His Ser Thr Val Asp Phe Arg Val Lys Ala Glu Asp Thr Val Thr Val

50

55

60

Glu Asn Val Leu Lys Gln Asn Glu Leu Gln Tyr Lys Val Leu Ile Ser

35

65

70

75

80

Asn Leu Arg Asn Val Val Glu Ala Gln Phe Asp Ser Arg Val Arg Leu

85

90

95



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(2) INFORMATION FOR SEQ ID NO: 115:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 520 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

60 GAGCTCGGCT AGCACCAAGG GCCCATCGGT CTTCCCCCTG GCGCCCTGCT CCAGGAGCAC

20 CTCTGGGGGC ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC 120

GGTGTCTGG AACTCAGGCG CCCTGACCAG CGGCGTGAC ACCTTCCCGG CTGTCCTACA 180

GTCCTCAGGA CTCTACTCCC TCAGCAGCGT GGTGACCGTG CCCTCCAGCA GCTTGGGCAC 240

25 CCAGACCTAC ACCTGCAACG TGAATCACAA GCCCAGCAAC ACCAAGGTGG ACAAGAGAGT 300

GGAGCTGAAA ACCCCACTCG GTGACACAAC TCACACGTGC CCTAGGTGTC CTGAACCTAA 360

30 ATCTTGTGAC ACACCTCCCC CGTGCCACAG GTGCCAGAG CCCAAATCTT GCGACACGCC 420

CCCACCGTGT CCCAGATGTC CTGAACCAA GAGCTGTGAC ACTCCACCGC CCTGCCCCGAG 480

GTGCCAGCA CCTGAAGTCC TGGGAGGGTA ATAGCCCGGG 520

35

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

- 178 -

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: other nucleic acid

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

GTTATTACTC GCTGCCCAAC CAGCCATGGC G

31

15 (2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

30 GCAGCAGGAT AGATTGTTGT AGC

23

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 88 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- 179 -

(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

CCGGAATTCT TATTAGTTCA GGTCTCCTC AGAGATCAGC TTCTGCTCCT CGAACTCATG 60

10

GTGGTGATGG TGGTGGTACA GGTGTTCC 88

(2) INFORMATION FOR SEQ ID NO: 119:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

CAATCTATCC TGCTGCTGGG ACTTCTAAAG 30

30 (2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- 180 -

(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

GATTGTTGTA GCTCCCGGGC

20

10 (2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

25 GGAGCTACAA CAATCTATCC TTCTGCTGGG

30

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

- 181 -

ACGGCACCAA GTACACATAT GG

22

(2) INFORMATION FOR SEQ ID NO: 123:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

ACGAGAATTC GACCGCTCTG CTGCAGCTGC ACCTCGGAAC CGCCACCGCT GCCACCGCCA

60

20 GAACCGCCAC CGTACAGGTG TTCCAGGACG

90

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 2154 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

35 ATGTTGGCAC TCTTGTTCT GGTGACTGTG GCCCTGGCAT CTGCTCATCA TGGTGGTGAG

60

CACTTTGAAG GCGAGAAGGT GTTCCGTGTT AACGTTGAAG ATGAAAATCA CATTACATA

120

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ATCCGCGAGT TGGCCAGCAC GACCCAGATT GACTTCTGGA AGCCAGATTC TGTCACACAA 180

ATCAAACCTC ACAGTACAGT TGA CTTCCTGT GTTAAAGCAG AAGATACTGT CACTGTGGAG 240

5 AATGTTCTAA AGCAGAATGA ACTACAATAC AAGGTACTGA TAAGCAACCT GAGAAATGTG 300

GTGGAGGCTC AGTTTGATAG CCGGGTTCGT GCAACAGGAC ACAGTTATGA GAAGTACAAC 360

AAGTGGGAAA CGATAGAGGC TTGGACTCAA CAAGTCGCCA CTGAGAATCC AGCCCTCATC 420

10 TCTCGCAGTG TTATCGGAAC CACATTGAG GGACGCGCTA TTTACCTCCT GAAGGTTGGC 480

AAAGCTGGAC AAAATAAGCC TGCCATTTTC ATGGACTGTG GTTTCCATGC CAGAGAGTGG 540

15 ATTTCTCCTG CATTCTGCCA GTGGTTTGTA AGAGAGGCTG TTCGTACCTA TGGACGTGAG 600

ATCCAAGTGA CAGAGCTTCT CGACAAGTTA GACTTTTATG TCCTGCCTGT GCTCAATATT 660

GATGGCTACA TCTACACCTG GACCAAGAGC CGATTTTGGA GAAAGACTCG CTCCACCCAT 720

20 ACTGGATCTA GCTGCATTGG CACAGACCCC AACAGAAATT TTGATGCTGG TTGGTGTGAA 780

ATTGGAGCCT CTCGAAACCC CTGTGATGAA ACTTACTGTG GACCTGCCGC AGAGTCTGAA 840

25 AAGGAGACCA AGGCCCTGGC TGATTTCATC CGCAACAAAC TCTCTTCCAT CAAGGCATAT 900

CTGACAATCC ACTCGTACTC CCAAATGATG ATCTACCCTT ACTCATATGC TTACAAACTC 960

GGTGAGAAC AATGCTGAGTT GAATGCCCTG GCTAAAGCTA CTGTGAAAGA ACTTGCCTCA 1020

30 CTGCACGGCA CCAAGTACAC ATATGGCCCG GGAGCTACAA CAATCTATCC TTCTGCTGGG 1080

ACTTCTAAAG ACTGGGCTTA TGACCAAGGA ATCAGATATT CCTTCACCTT TGA ACTTCGA 1140

35 GATACAGGCA GATATGGCTT TCTCCTTCCA GAATCCCAGA TCCGGGCTAC CTGCGAGGAG 1200

ACCTTCCTGG CAATCAAGTA TGTGCCCAGC TACGTCCTGG AACACCTGTA CGGTGGCGGT 1260

- 183 -

TCTGGCGGTG GCAGCGGTGG CGGTTCCGAG GTGCAGCTGC AGCAGAGCGG TCCAGGTCTC 1320

GTACGGCCTA GCCAGACCCT GAGCCTCAGC TGCACCGCAT CTGGCTTCAA CATTAAGGAC 1380

5 AATTACATGC ACTGGGTGAG ACAGCCACCT GGACGAGGCC TTGAGTGGAT TGGATGGATT 1440

GACCCTGAGA ATGGTGACAC TGAGTACGCA CCTAAGTTTC GCGGCCGCGT GACAATGCTG 1500

GCAGACACTA GTAAGAACCA GTTCAGCCTG AGACTCAGCA GCGTGACAGC CGCCGACACC 1560

10 GCGGTCTATT ATTGTCACGT CCTGATATAC GCCGGGTATC TGGCAATGGA CTACTGGGGC 1620

CAAGGGACCC TCGTCACCGT GAGCTCGGCT AGCACCAAGG GCCCATCGGT CTTCCCCCTG 1680

15 GCGCCCTGCT CCAGGAGCAC CTCTGGGGGC ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC 1740

TACTTCCCCG AACCGGTGAC GGTGTCGTGG AACTCAGGCG CCCTGACCAG CGGCGTGAC 1800

ACCTTCCCCG CTGTCCTACA GTCCTCAGGA CTCTACTCCC TCAGCAGCGT GGTGACCGTG 1860

20 CCCTCCAGCA GCTTGGGCAC CCAGACCTAC ACCTGCAACG TGAATCACA GCCCAGCAAC 1920

ACCAAGGTGG ACAAGAGAGT GGAGCTGAAA ACCCCACTCG GTGACACAAC TCACACGTGC 1980

25 CCTAGGTGTC CTGAACCTAA ATCTTGTGAC ACACCTCCCC CGTGCCCACG GTGCCCAGAG 2040

CCCAAATCTT GCGACACGCC CCCACCGTGT CCCAGATGTC CTGAACCAAA GAGCTGTGAC 2100

ACTCCACCGC CTGCCCCGAG GTGCCAGCA CCTGAACTCC TGGGAGGGTA ATAG 2154

30

(2) INFORMATION FOR SEQ ID NO: 125:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 716 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- 184 -

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

Met Leu Ala Leu Leu Val Leu Val Thr Val Ala Leu Ala Ser Ala His

1 5 10 15

His Gly Gly Glu His Phe Glu Gly Glu Lys Val Phe Arg Val Asn Val

20 25 30

Glu Asp Glu Asn His Ile Asn Ile Ile Arg Glu Leu Ala Ser Thr Thr

35 40 45

Gln Ile Asp Phe Trp Lys Pro Asp Ser Val Thr Gln Ile Lys Pro His

50 55 60

Ser Thr Val Asp Phe Arg Val Lys Ala Glu Asp Thr Val Thr Val Glu

65 70 75 80

Asn Val Leu Lys Gln Asn Glu Leu Gln Tyr Lys Val Leu Ile Ser Asn

85 90 95

Leu Arg Asn Val Val Glu Ala Gln Phe Asp Ser Arg Val Arg Ala Thr

100 105 110

Gly His Ser Tyr Glu Lys Tyr Asn Lys Trp Glu Thr Ile Glu Ala Trp

115 120 125

Thr Gln Gln Val Ala Thr Glu Asn Pro Ala Leu Ile Ser Arg Ser Val

130 135 140

Ile Gly Thr Thr Phe Glu Gly Arg Ala Ile Tyr Leu Leu Lys Val Gly

145 150 155 160



- 185 -

Lys Ala Gly Gln Asn Lys Pro Ala Ile Phe Met Asp Cys Gly Phe His  
 165 170 175

5 Ala Arg Glu Trp Ile Ser Pro Ala Phe Cys Gln Trp Phe Val Arg Glu  
 180 185 190

Ala Val Arg Thr Tyr Gly Arg Glu Ile Gln Val Thr Glu Leu Leu Asp  
 195 200 205

10 Lys Leu Asp Phe Tyr Val Leu Pro Val Leu Asn Ile Asp Gly Tyr Ile  
 210 215 220

15 Tyr Thr Trp Thr Lys Ser Arg Phe Trp Arg Lys Thr Arg Ser Thr His  
 225 230 235 240

Thr Gly Ser Ser Cys Ile Gly Thr Asp Pro Asn Arg Asn Phe Asp Ala  
 245 250 255

20 Gly Trp Cys Glu Ile Gly Ala Ser Arg Asn Pro Cys Asp Glu Thr Tyr  
 260 265 270

Cys Gly Pro Ala Ala Glu Ser Glu Lys Glu Thr Lys Ala Leu Ala Asp  
 275 280 285

25 Phe Ile Arg Asn Lys Leu Ser Ser Ile Lys Ala Tyr Leu Thr Ile His  
 290 295 300

Ser Tyr Ser Gln Met Met Ile Tyr Pro Tyr Ser Tyr Ala Tyr Lys Leu  
 305 310 315 320

30 Gly Glu Asn Asn Ala Glu Leu Asn Ala Leu Ala Lys Ala Thr Val Lys  
 325 330 335

35 Glu Leu Ala Ser Leu His Gly Thr Lys Tyr Thr Tyr Gly Pro Gly Ala  
 340 345 350

Thr Thr Ile Tyr Pro Ser Ala Gly Thr Ser Lys Asp Trp Ala Tyr Asp  
 355 360 365

- 186 -

Gln Gly Ile Arg Tyr Ser Phe Thr Phe Glu Leu Arg Asp Thr Gly Arg  
 370 375 380

5 Tyr Gly Phe Leu Leu Pro Glu Ser Gln Ile Arg Ala Thr Cys Glu Glu  
 385 390 395 400

Thr Phe Leu Ala Ile Lys Tyr Val Ala Ser Tyr Val Leu Glu His Leu  
 405 410 415

10 Tyr Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln  
 420 425 430

15 Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln Thr Leu Ser  
 435 440 445

Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn Tyr Met His  
 450 455 460

20 Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile Gly Trp Ile  
 465 470 475 480

Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe Arg Gly Arg  
 485 490 495

25 Val Thr Met Leu Ala Asp Thr Ser Lys Asn Gln Phe Ser Leu Arg Leu  
 500 505 510

30 Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys His Val Leu  
 515 520 525

Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu  
 530 535 540

35 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
 545 550 555 560

- 187 -

Ala Pro Cys Ser Arg Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
 565 570 575

5 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
 580 585 590

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
 595 600 605

10 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
 610 615 620

15 Leu Gly Thr Gln Thr Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn  
 625 630 635 640

Thr Lys Val Asp Lys Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr  
 645 650 655

20 Thr His Thr Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro  
 660 665 670

Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro  
 675 680 685

25 Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro  
 690 695 700

Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu Gly Gly  
 705 710 715

30

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 42 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- 188 -

(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

TATATAAAGC TTGCCGCCAC CATGGGCCAC ACACGGAGGC AG

42

10 (2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

15

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

25 ACTCCACCAG CTTACCTCG TTATCAGGAA AATGCTCTTG CTTGG

45

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: other nucleic acid

- 189 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

AGAGCATTTT CCTGATAACG AGGTGAAGCT GGTGGAGTCT GGAGG

45

5

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

CCAGGCATCC CAGGGTCACC ATGGAGTTAG TTTGGGCAGC

40

20

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1446 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25

30

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:16..1435

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

AAGCTTGCCG CCACC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA TCC 51  
 Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser  
 5 1 5 10

AAG TGT CCA TAC CTC AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT CTT 99  
 Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu  
 15 20 25

10  
 TCT CAC TTC TGT TCA GGT GTT ATC CAC GTG ACC AAG GAA GTG AAA GAA 147  
 Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu  
 30 35 40

15 GTG GCA ACG CTG TCC TGT GGT CAC AAT GTT TCT GTT GAA GAG CTG GCA 195  
 Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala  
 45 50 55 60

CAA ACT CGC ATC TAC TGG CAA AAG GAG AAG AAA ATG GTG CTG ACT ATG 243  
 20 Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met  
 65 70 75

ATG TCT GGG GAC ATG AAT ATA TGG CCC GAG TAC AAG AAC CGG ACC ATC 291  
 Met Ser Gly Asp Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile  
 25 80 85 90

TTT GAT ATC ACT AAT AAC CTC TCC ATT GTG ATC CTG GCT CTG CGC CCA 339  
 Phe Asp Ile Thr Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro  
 95 100 105

30  
 TCT GAC GAG GGC ACA TAC GAG TGT GTT GTT CTG AAG TAT GAA AAA GAC 387  
 Ser Asp Glu Gly Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp  
 110 115 120

35 GCT TTC AAG CGG GAA CAC CTG GCT GAA GTG ACG TTA TCA GTC AAA GCT 435  
 Ala Phe Lys Arg Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala  
 125 130 135 140

- 191 -

	GAC TTC CCT ACA CCT AGT ATA TCT GAC TTT GAA ATT CCA ACT TCT AAT	483
	Asp Phe Pro Thr Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn	
	145 150 155	
5	ATT AGA AGG ATA ATT TGC TCA ACC TCT GGA GGT TTT CCA GAG CCT CAC	531
	Ile Arg Arg Ile Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His	
	160 165 170	
	CTC TCC TGG TTG GAA AAT GGA GAA GAA TTA AAT GCC ATC AAC ACA ACA	579
10	Leu Ser Trp Leu Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr	
	175 180 185	
	GTT TCC CAA GAT CCT GAA ACT GAG CTC TAT GCT GTT AGC AGC AAA CTG	627
	Val Ser Gln Asp Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu	
15	190 195 200	
	GAT TTC AAT ATG ACA ACC AAC CAC AGC TTC ATG TGT CTC ATC AAG TAT	675
	Asp Phe Asn Met Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr	
	205 210 215 220	
20		
	GGA CAT TTA AGA GTG AAT CAG ACC TTC AAC TGG AAT ACA ACC AAG CAA	723
	Gly His Leu Arg Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln	
	225 230 235	
25	GAG CAT TTT CCT GAT AAC GAG GTG AAG CTG GTG GAG TCT GGA GGA GGC	771
	Glu His Phe Pro Asp Asn Glu Val Lys Leu Val Glu Ser Gly Gly Gly	
	240 245 250	
30	TTG GTA CAG CCT GGG GGT TCT CTG AGA CTC TCC TGT GCA ACT TCT GGG	819
	Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly	
	255 260 265	
	TTC ACC TTC ACT GAT TAC TAC ATG AAC TGG GTC CGC CAG CCT CCA GGA	867
35	Phe Thr Phe Thr Asp Tyr Tyr Met Asn Trp Val Arg Gln Pro Pro Gly	
	270 275 280	
	AAG GCA CTT GAG TGG TTG GGT TTT ATT GGA AAC AAA GCT AAT GGT TAC	915

Lys Ala Leu Glu Trp Leu Gly Phe Ile Gly Asn Lys Ala Asn Gly Tyr  
285 290 295 300

ACA ACA GAG TAC AGT GCA TCT GTG AAG GGT CGG TTC ACC ATC TCC AGA 963  
5 Thr Thr Glu Tyr Ser Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg  
305 310 315

GAC AAA TCC CAA AGC ATC CTC TAT CTT CAA ATG AAC ACC CTG AGA GCT 1011  
Asp Lys Ser Gln Ser Ile Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala  
10 320 325 330

GAG GAC AGT GCC ACT TAT TAC TGT ACA AGA GAT AGG GGG CTA CGG TTC 1059  
Glu Asp Ser Ala Thr Tyr Tyr Cys Thr Arg Asp Arg Gly Leu Arg Phe  
335 340 345

15

TAC TTT GAC TAC TGG GGC CAA GGC ACC ACT CTC ACA GTC TCC TCA GCC 1107

Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala

350 355 360

20 AAA ACG ACA CCC CCA TCT GTC TAT CCA CTG GCC CCT GGA TCT GCT GCC 1155  
Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala  
365 370 375 380

CAA ACT AAC TCC ATG GTG ACC CTG GGA TGC CTG GTC AAG GGC TAT TTC 1203  
25 Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe  
385 390 395

CCT GAG CCA GTG ACA GTG ACC TGG AAC TCT GGA TCT CTG TCC AGC GGT 1251  
Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly  
30 400 405 410

GTG	CAC	ACC	TTC	CCA	GCT	GTC	CTG	CAG	TCT	GAC	CTC	TAC	ACT	CTG	AGC	1299
Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Asp	Leu	Tyr	Thr	Leu	Ser	
415			420			425										

35

AGC TCA GTG ACT GTC CCC TCC AGC ACC TGG CCC AGC GAG ACC GTC ACC 1347

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr

430 435 440



- 193 -

TGC AAC GTT GCC CAC CCG GCC AGC AGC ACC AAG GTG GAC AAG AAA ATT 1395  
 Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile  
 445 450 455 460

5

GTG CCC AGG GAT TGT GGT TGT AAG CCT TGC ATA TGT ACA T AGTAAGAATT 1445  
 Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr  
 465 470

10 c

1446

(2) INFORMATION FOR SEQ ID NO: 131:

15

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 473 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr  
 1 5 10 15

25

Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys  
 20 25 30

30

Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu  
 35 40 45

Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile  
 50 55 60

35

Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp  
 65 70 75 80

Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr  
85 90 95

Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg  
115 120 125

Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile  
145                      150                      155                      160

Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp  
180 185 190

25 Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg  
210 215 220

Asp Asn Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro  
245 250 255

35 Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Thr  
260 265 270

- 195 -

Trp Leu Gly Phe Ile Gly Asn Lys Ala Asn Gly Tyr Thr Thr Glu Tyr  
-290                      295                      300

Ser Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Gln  
305                    310                    315                    320

10 Ser Ile Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala Glu Asp Ser Ala  
325 330 335

Thr Tyr Tyr Cys Thr Arg Asp Arg Gly Leu Arg Phe Tyr Phe Asp Tyr  
340 345 350

15

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro

355 360 365

Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser  
20            370                            375                            380

Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val  
385                      390                      395                      400

25 Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe  
405 410 415

Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr  
420 425 430

30  
Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala  
435 440 445

His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp  
35            450                    455                            460

Cys Gly Cys Lys Pro Cys Ile Cys Thr  
465 470